

SEQUENCE LISTING

<110> FAGAN, RICHARD JOSEPH
 PHELPS, CHRISTOPHER BENJAMIN
 RODRIGUES, TANIA MARTA
 POWER, CHRISTINE
 BIENKOWSKA, JADWIGA

<120> Metalloprotease Proteins

<130> C.R.107

<140> US 10/539,847
 <141> 2005-06-20

<150> GB 0230006.9
 <151> 2002-12-23

<160> 66

<170> SeqWin99, version 1.02

<210> 1
 <211> 52
 <212> DNA
 <213> Homo sapiens

<400> 1
 atgggtggtgta gtgggtgctgt ggaggtcccc ttctgtctct ccagcaagta cg 52

<210> 2
 <211> 18
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Gly Gly Ser Gly Val Val Glu Val Pro Phe Leu Leu Ser Ser Lys
 1 5 10 15

Tyr Asp

<210> 3
 <211> 118
 <212> DNA
 <213> Homo sapiens

<400> 3
 atgagcccgag ccgcccaggtc atcctggagg ctcttgcgga gtttgaacgt tccacgtgca 60
 tcagggtttgt cacctatcag gaccagagag acttcatttc catcatcccc atgtatgg 118

<210> 4
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 4
 Glu Pro Ser Arg Gln Val Ile Leu Glu Ala Leu Ala Glu Phe Glu Arg
 1 5 10 15
 Ser Thr Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp Phe Ile
 20 25 30
 Ser Ile Ile Pro Met Tyr Gly
 35

<210> 5
 <211> 182
 <212> DNA
 <213> Homo sapiens

<400> 5
 gtgcttctcg agtgtggggc gcagtgagg gatgcagggtg gtctccctgg cggccacgtg 60
 tctccagaag ggccggggca ttgtccttca tgagctcatg catgtgctgg gcttctggca 120
 cgagcaacacg cgggcccacc gggaccgcta tatccgtgtc aactggaacg agatcctgcc 180
 ag 182

<210> 6
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 6
 Cys Phe Ser Ser Val Gly Arg Ser Gly Gly Met Gln Val Val Ser Leu
 1 5 10 15
 Ala Pro Thr Cys Leu Gln Lys Gly Arg Gly Ile Val Leu His Glu Leu
 20 25 30
 Met His Val Leu Gly Phe Trp His Glu His Thr Arg Ala Asp Arg Asp
 35 40 45
 Arg Tyr Ile Arg Val Asn Trp Asn Glu Ile Leu Pro Gly
 50 55 60

<210> 7
 <211> 82
 <212> DNA
 <213> Homo sapiens

<400> 7
 gctttgaaat caacttcac aagtctcaga gcagcaacat gctgacgcc tatgactact 60
 cctctgtgat gcactatggg ag 82

<210> 8
 <211> 27
 <212> PRT
 <213> Homo sapiens

<400> 8

Phe Glu Ile Asn Phe Ile Lys Ser Gln Ser Ser Asn Met Leu Thr Pro
 1 5 10 15

Tyr Asp Tyr Ser Ser Val Met His Tyr Gly Arg
 20 25

<210> 9
 <211> 155
 <212> DNA
 <213> Homo sapiens
 <400> 9
 gctcgccttc agccggcgtg ggetgcccac catcacacca ctttggggccc ccagtgtcca 60
 catcggccag ccatggaacc tgagtgcctc ggacatcacc cgggtcctca aactctacgg 120
 ctgcagccca agtggcccca ggcctcgtgg gagag 155

<210> 10
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 10
 Leu Ala Phe Ser Arg Arg Gly Leu Pro Thr Ile Thr Pro Leu Trp Ala
 1 5 10 15

Pro Ser Val His Ile Gly Gln Arg Trp Asn Leu Ser Ala Ser Asp Ile
 20 25 30

Thr Arg Val Leu Lys Leu Tyr Gly Cys Ser Pro Ser Gly Pro Arg Pro
 35 40 45

Arg Gly Arg Gly
 50

<210> 11
 <211> 419
 <212> DNA
 <213> Homo sapiens
 <400> 11
 ggtcccatgc ccacagcact ggtaggagcc ccgccccggc ctccctatct ctgcagcggc 60
 ttttgagggc actgtcggcg gaatccagga gccccgaccc cagtggttcc agtgcgggag 120
 gccagcccggt tctgtcaggg cctggggaga gccacatag gtgggagtc cctgccctga 180
 aaaagctcag tgcagaggcc toggcaaggc agcctcagac cctagcttcc tcccaagat 240
 caaggcctgg agcaggtgcc cccggtgttg ctccaggagca gtccctgggtg gccggagtg 300
 ccaccaagcc cacagtccca tcttcagaag cagggaatcca gccagtcctt gtccagggaa 360
 gccagctctt gccagggggc tgtgtacctt gaaatcattt caaggggatg tccgaagat 419

<210> 12
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 12
 Ser His Ala His Ser Thr Arg Ser Pro Ala Pro Ala Ser Leu Ser

1	5	10	15
Leu Gln Arg	Leu Leu Glu Ala Leu Ser Ala Glu Ser Arg Ser Pro Asp		
	20	25	30
Pro Ser Gly Ser Ser Ala Gly Gly Gln Pro Val Pro Ala Gly Pro Gly			
	35	40	45
Glu Ser Pro His Gly Trp Glu Ser Pro Ala Leu Lys Lys Leu Ser Ala			
	50	55	60
Glu Ala Ser Ala Arg Gln Pro Gln Thr Leu Ala Ser Ser Pro Arg Ser			
	65	70	75
Arg Pro Gly Ala Gly Ala Pro Gly Val Ala Gln Glu Gln Ser Trp Leu			
	85	90	95
Ala Gly Val Ser Thr Lys Pro Thr Val Pro Ser Ser Glu Ala Gly Ile			
	100	105	110
Gln Pro Val Pro Val Gln Gly Ser Pro Ala Leu Pro Gly Gly Cys Val			
	115	120	125
Pro Arg Asn His Phe Lys Gly Met Ser Glu Asp			
	130	135	

<210> 13
 <211> 1008
 <212> DNA
 <213> Homo sapiens

<400> 13	
atgggttggtg	gtggtgtcgt ggagggtcccc ttcctgtctt ccagcaagta cgtatgagccc 60
agccgccagg	tcattcttga ggctcttgcc gagtttgaac gttccacgtg catcagggttt 120
gtcacctatc	aggaccagag agacttcatt tccatcatcc ccattgtatgg gtgcttctcg 180
agtgtggggc	cgactggagg gatgcagggt gtctccctgg cgcgccacgtg tctccagaag 240
ggccggggca	ttgtccctca tgagctcatg catgtgtcgt gcttctggca cgagcacacg 300
cgggccgacc	gggaccgcta tatcctgttc aactggaacg agatctctgc aggtcttgaa 360
atcaacttca	tcaaagtctca gacgagcaac atgtcgaacg cctatgacta ctctctctgtg 420
atgcactatg	ggaggctcgc cttcagccgg cgtgggctgc ccaccatcac accactttgg 480
gccccacgtg	tcacatcagg ccagcgatgg aacctgagtg cctcggacat caccgggtgc 540
ctcaaaactct	acggctgcag cccaagtggc ccaggccccc gtgggagagg gtcccatgcc 600
cacagcactg	gtaggagccc cgcgccggcc tccctatctc tgcagcggtc ttggaggaac 660
ctgtcggcgg	aatccaggag ccccgacccc agtgggttcca gtgcgggagg ccagcccggtt 720
cctgcagggc	ctggggagag cccacatggg tgggagtcgc gtgccctgaa aaagctcagt 780
gcagaggcct	cggaaggcca gccctcagacc ctatgcttct ccccaagatc aaggcctgga 840
gcaggtgtccc	ccgtgtttgc tcaggagcag tctgtgctgg ccggagtgtc caccagccc 900
acagtcocat	cttcagaagc aggaatccag ccagtccctg tccagggaag ccagctctg 960
ccagggggtc	gtgtacataa aaatcatctt aaggggatgt ccgaagat 1008

<210> 14
 <211> 336
 <212> PRT
 <213> Homo sapiens

```

<400> 14
Met Gly Gly Ser Gly Val Val Glu Val Pro Phe Leu Leu Ser Ser Lys
1 5 10 15
Tyr Asp Glu Pro Ser Arg Gln Val Ile Leu Glu Ala Leu Ala Glu Phe
20 25 30
Glu Arg Ser Thr Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp
35 40 45
Phe Ile Ser Ile Ile Pro Met Tyr Gly Cys Phe Ser Ser Val Gly Arg
50 55 60
Ser Gly Gly Met Gln Val Val Ser Leu Ala Pro Thr Cys Leu Gln Lys
65 70 75 80
Gly Arg Gly Ile Val Leu His Glu Leu Met His Val Leu Gly Phe Trp
85 90 95
His Glu His Thr Arg Ala Asp Arg Asp Arg Tyr Ile Arg Val Asn Trp
100 105 110
Asn Glu Ile Leu Pro Gly Phe Glu Ile Asn Phe Ile Lys Ser Gln Ser
115 120 125
Ser Asn Met Leu Thr Pro Tyr Asp Tyr Ser Ser Val Met His Tyr Gly
130 135 140
Arg Leu Ala Phe Ser Arg Arg Gly Leu Pro Thr Ile Thr Pro Leu Trp
145 150 155 160
Ala Pro Ser Val His Ile Gly Gln Arg Trp Asn Leu Ser Ala Ser Asp
165 170 175
Ile Thr Arg Val Leu Lys Leu Tyr Gly Cys Ser Pro Ser Gly Pro Arg
180 185 190
Pro Arg Gly Arg Gly Ser His Ala His Ser Thr Gly Arg Ser Pro Ala
195 200 205
Pro Ala Ser Leu Ser Leu Gln Arg Leu Leu Glu Ala Leu Ser Ala Glu
210 215 220
Ser Arg Ser Pro Asp Pro Ser Gly Ser Ser Ala Gly Gly Gln Pro Val
225 230 235 240
Pro Ala Gly Pro Gly Glu Ser Pro His Gly Trp Glu Ser Pro Ala Leu
245 250 255
Lys Lys Leu Ser Ala Glu Ala Ser Ala Arg Gln Pro Gln Thr Leu Ala
260 265 270
Ser Ser Pro Arg Ser Arg Pro Gly Ala Gly Ala Pro Gly Val Ala Gln
275 280 285

```

Glu Gln Ser Trp Leu Ala Gly Val Ser Thr Lys Pro Thr Val Pro Ser
 290 295 300

Ser Glu Ala Gly Ile Gln Pro Val Pro Val Gln Gly Ser Pro Ala Leu
 305 310 315 320

Pro Gly Gly Cys Val Pro Arg Asn His Phe Lys Gly Met Ser Glu Asp
 325 330 335

<210> 15
 <211> 55
 <212> DNA
 <213> Homo sapiens

<400> 15
 atggagggtg taggggggtct ctggccttgg gtgctgggtc tgctctcctt gccag 55

<210> 16
 <211> 19
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Glu Gly Val Gly Gly Leu Trp Pro Trp Val Leu Gly Leu Leu Ser
 1 5 10 15

Leu Pro Gly

<210> 17
 <211> 126
 <212> DNA
 <213> Homo sapiens

<400> 17
 gtgtgatcct aggagcgccc ctggcctcca gctgcgcagg agcctgtggt accagcttcc 60
 cagatggcct cacccttgag ggaaccgagg cctccgggga caaggacatt cctgcaatta 120
 accaag 126

<210> 18
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 18
 Val Ile Leu Gly Ala Pro Leu Ala Ser Ser Cys Ala Gly Ala Cys Gly
 1 5 10 15

Thr Ser Phe Pro Asp Gly Leu Thr Pro Glu Gly Thr Gln Ala Ser Gly
 20 25 30

Asp Lys Asp Ile Pro Ala Ile Asn Gln Gly
 35 40

<210> 19
 <211> 62
 <212> DNA
 <213> Homo sapiens

<400> 19
 ggctcctcct ggaagaaacc ccagagagca gcttcctcat cgagggggac atcatccggc 60
 cg 62

<210> 20
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 20
 Leu Ile Leu Glu Glu Thr Pro Glu Ser Ser Phe Leu Ile Glu Gly Asp
 1 5 10 15

Ile Ile Arg Pro
 20

<210> 21
 <211> 94
 <212> DNA
 <213> Homo sapiens

<400> 21
 agtcccttcc gactgctgtc agcaaccagc aacaaatggc ccattgggtgg tagtgggtgc 60
 gtggagggtc ccttcctgct ctccagcaag tacg 94

<210> 22
 <211> 32
 <212> PRT
 <213> Homo sapiens

<400> 22
 Ser Pro Phe Arg Leu Leu Ser Ala Thr Ser Asn Lys Trp Pro Met Gly
 1 5 10 15

Gly Ser Gly Val Val Glu Val Pro Phe Leu Leu Ser Ser Lys Tyr Asp
 20 25 30

<210> 23
 <211> 118
 <212> DNA
 <213> Homo sapiens

<400> 23
 atgagcccag ccgcagagtc atcctggagg ctcttgcgga gtttgaacgt tccacgtgca 60
 tcaggtttgt cacctatcag gaccagagag acttcatttc catcatcccc atgtatgg 118

<210> 24
 <211> 39
 <212> PRT

<213> Homo sapiens

<400> 24

Glu Pro Ser Arg Gln Val Ile Leu Glu Ala Leu Ala Glu Phe Glu Arg
1 5 10 15

Ser Thr Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp Phe Ile
20 25 30

Ser Ile Ile Pro Met Tyr Gly
35

<210> 25

<211> 182

<212> DNA

<213> Homo sapiens

<400> 25

gtgcttctcg agtgtggggc gcagtggagg gatgcagggtg gtctccctgg cgcccacgtg 60
tctccagaag gcccggggca ttgtccttca tgagctcatg catgtgtctgg gcttctggca 120
cgagcacacg cgggcccagc gggaccgcta tatccgtgtc aactggaacg agatcctgcc 180
ag 182

<210> 26

<211> 61

<212> PRT

<213> Homo sapiens

<400> 26

Cys Phe Ser Ser Val Gly Arg Ser Gly Gly Met Gln Val Val Ser Leu
1 5 10 15

Ala Pro Thr Cys Leu Gln Lys Gly Arg Gly Ile Val Leu His Glu Leu
20 25 30

Met His Val Leu Gly Phe Trp His Glu His Thr Arg Ala Asp Arg Asp
35 40 45

Arg Tyr Ile Arg Val Asn Trp Asn Glu Ile Leu Pro Gly
50 55 60

<210> 27

<211> 82

<212> DNA

<213> Homo sapiens

<400> 27

gctttgaaat caacttcate aagtctcgga gcagcaacat gctgacgcc tatgactact 60
cctctgtgat gcactatggg ag 82

<210> 28

<211> 27

<212> PRT

<213> Homo sapiens

<400> 28
 Phe Glu Ile Asn Phe Ile Lys Ser Arg Ser Ser Asn Met Leu Thr Pro
 1 5 10 15

Tyr Asp Tyr Ser Ser Val Met His Tyr Gly Arg
 20 25

<210> 29
 <211> 155
 <212> DNA
 <213> Homo sapiens

<400> 29
 gctcgccctc agccggcggtg ggctgcccac catcacacca ctttgggccc ccagtggtcca 60
 catcgccag cgatggaacc tgagtgcctc ggacatcacc cgggtcctca aaclctacgg 120
 ctgcagccca agtggcccca ggcccgtgg gagag 155

<210> 30
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 30
 Leu Ala Phe Ser Arg Arg Gly Leu Pro Thr Ile Thr Pro Leu Trp Ala
 1 5 10 15

Pro Ser Val His Ile Gly Gln Arg Trp Asn Leu Ser Ala Ser Asp Ile
 20 25 30

Thr Arg Val Leu Lys Leu Tyr Gly Cys Ser Pro Ser Gly Pro Arg Pro
 35 40 45

Arg Gly Arg Gly
 50

<210> 31
 <211> 419
 <212> DNA
 <213> Homo sapiens

<400> 31
 ggtcccatgc ccacagcaact ggtaggagcc ccgctccggc ctccttatct ctgcagcgcc 60
 ttttgagggc actgtcggcg gaatccagga gccccgaccc cagtgggtcc agtgcgggag 120
 gccagccnct tccgtcaggg cctggggaga gccacatgg gtgggagtc cctgcctga 180
 aaaagctcag tgcagagggc tcggcaaggc agcctcagac cctagcttcc tccccaagat 240
 caaggcctgg agcaggtgcc ccgggtgttg ctcaggagca gtccctgggtg gccggagtg 300
 ccaccaagcc caccagtcca tcttcagaag caggaatcca gccagtccct gtccagggaa 360
 gccagctct gccagggggc tgtgtacctt gaaatcattt caaggggatg tccgaagat 419

<210> 32
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 32

Ser His Ala His Ser Thr Gly Arg Ser Pro Ala Pro Ala Ser Leu Ser
1 5 10 15

Leu Gln Arg Leu Leu Glu Ala Leu Ser Ala Glu Ser Arg Ser Pro Asp
20 25 30

Pro Ser Gly Ser Ser Ala Gly Gly Gln Pro Val Pro Ala Gly Pro Gly
35 40 45

Glu Ser Pro His Gly Trp Glu Ser Pro Ala Leu Lys Lys Leu Ser Ala
50 55 60

Glu Ala Ser Ala Arg Gln Pro Gln Thr Leu Ala Ser Ser Pro Arg Ser
65 70 75 80

Arg Pro Gly Ala Gly Ala Pro Gly Val Ala Gln Glu Gln Ser Trp Leu
85 90 95

Ala Gly Val Ser Thr Lys Pro Thr Val Pro Ser Ser Glu Ala Gly Ile
100 105 110

Gln Pro Val Pro Val Gln Gly Ser Pro Ala Leu Pro Gly Gly Cys Val
115 120 125

Pro Arg Asn His Phe Lys Gly Met Ser Glu Asp
130 135

<210> 33
<211> 1293
<212> DNA
<213> Homo sapiens

<400> 33
atggagggtg taggggggtct ctggccttgg gtgctgggtc tgcctcctct gccaggtgtg 60
atccttaggag cgcctctggc ctccagctgc gcaggagcct gtggtaccag cttccagat 120
ggcctcacc ctaggggaac ccaggcctcc ggggacaagg acattcctgc aatlaaccaa 180
gggctcctcc tggaaagaac ccagagagag agcttctcca tcgaggggag catcatccgg 240
ccgagtcctt tccgactgct gtcagcaacc agcaacaaat ggccatggg tggtagtggt 300
gtcgtggagg tccccttctt gctctccagc aagtacgatg agcccagcc ccaggtcac 360
ctggaggctc ttgcggagtt tgaacgttcc acgtgcatac ggtttgtcac ctatcaggac 420
cagagagact tcatctccat catcccctat tatgggtgct tctcgatgtg gggcgccagt 480
ggagggatgc aggtggtctc cctggcgccc acgtgtctcc agaaggccg gggcattgtc 540
cttcatgagc tcatgcatgt gctgggcttc tggcagcagc acacgcgggc cgaccgggac 600
cgctatatcc gtgtcaactg gaacgagatc ctgccaggct ttgaaatcaa ctcatcaag 660
tctcggagca gcaacatgct gacgccctat gactactcct ctgtgatgca ctatgggagg 720
ctgcctctca gcgcgggtgg gctgccacc atcacaccac ttggggcccc cagtgtccac 780
atcgccagc gatggaaact gactgcctcg gacatcaacc ggtctctcaa actctacggc 840
tgacgcccaa gtggccccc gccccttggg agagggtccc atgccacag cactggtagg 900
agccccctc cggcctccct atctctgcag cggcttttgg aggcactgtc ggcggaatcc 960
aggagcccc accccagttg ttccagtgcg ggaggccaag cgttctctgc agggcctggg 1020
gagagccac atgggtggga gtccccctgc ctgaaaaagc tcagtgcaga ggccctcgca 1080
aggcagctc agaccctagc ttctcccca agatcaaggc ctggagcagg tgcccccggt 1140
gttctcagg agcagtcctg gctggccgga gtgtccacca agcccacagt cccatcttca 1200
gaagcaggaa tccagccagt cctgtccag ggaagccag ctctgccagg gggctgtgta 1260
ctagaaaatc atttcaagg gatgtccgaa gat 1293

```

<210> 34
<211> 431
<212> PRT
<213> Homo sapiens

<400> 34
Met Glu Gly Val Gly Gly Leu Trp Pro Trp Val Leu Gly Leu Leu Ser
1 5 10 15

Leu Pro Gly Val Ile Leu Gly Ala Pro Leu Ala Ser Ser Cys Ala Gly
20 25 30

Ala Cys Gly Thr Ser Phe Pro Asp Gly Leu Thr Pro Glu Gly Thr Gln
35 40 45

Ala Ser Gly Asp Lys Asp Ile Pro Ala Ile Asn Gln Gly Leu Ile Leu
50 55 60

Glu Glu Thr Pro Glu Ser Ser Phe Leu Ile Glu Gly Asp Ile Ile Arg
65 70 75 80

Pro Ser Pro Phe Arg Leu Leu Ser Ala Thr Ser Asn Lys Trp Pro Met
85 90 95

Gly Gly Ser Gly Val Val Glu Val Pro Phe Leu Leu Ser Ser Lys Tyr
100 105 110

Asp Glu Pro Ser Arg Gln Val Ile Leu Glu Ala Leu Ala Glu Phe Glu
115 120 125

Arg Ser Thr Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp Phe
130 135 140

Ile Ser Ile Ile Pro Met Tyr Gly Cys Phe Ser Ser Val Gly Arg Ser
145 150 155 160

Gly Gly Met Gln Val Val Ser Leu Ala Pro Thr Cys Leu Gln Lys Gly
165 170 175

Arg Gly Ile Val Leu His Glu Leu Met His Val Leu Gly Phe Trp His
180 185 190

Glu His Thr Arg Ala Asp Arg Asp Arg Tyr Ile Arg Val Asn Trp Asn
195 200 205

Glu Ile Leu Pro Gly Phe Glu Ile Asn Phe Ile Lys Ser Arg Ser Ser
210 215 220

Asn Met Leu Thr Pro Tyr Asp Tyr Ser Ser Val Met His Tyr Gly Arg
225 230 235 240

Leu Ala Phe Ser Arg Arg Gly Leu Pro Thr Ile Thr Pro Leu Trp Ala
245 250 255

```

Pro Ser Val His Ile Gly Gln Arg Trp Asn Leu Ser Ala Ser Asp Ile
 260 265 270

Thr Arg Val Leu Lys Leu Tyr Gly Cys Ser Pro Ser Gly Pro Arg Pro
 275 280 285

Arg Gly Arg Gly Ser His Ala His Ser Thr Gly Arg Ser Pro Ala Pro
 290 295 300

Ala Ser Leu Ser Leu Gln Arg Leu Leu Glu Ala Leu Ser Ala Glu Ser
 305 310 315 320

Arg Ser Pro Asp Pro Ser Gly Ser Ser Ala Gly Gly Gln Pro Val Pro
 325 330 335

Ala Gly Pro Gly Glu Ser Pro His Gly Trp Glu Ser Pro Ala Leu Lys
 340 345 350

Lys Leu Ser Ala Glu Ala Ser Ala Arg Gln Pro Gln Thr Leu Ala Ser
 355 360 365

Ser Pro Arg Ser Arg Pro Gly Ala Gly Ala Pro Gly Val Ala Gln Glu
 370 375 380

Gln Ser Trp Leu Ala Gly Val Ser Thr Lys Pro Thr Val Pro Ser Ser
 385 390 395 400

Glu Ala Gly Ile Gln Pro Val Pro Val Gln Gly Ser Pro Ala Leu Pro
 405 410 415

Gly Gly Cys Val Pro Arg Asn His Phe Lys Gly Met Ser Glu Asp
 420 425 430

<210> 35
 <211> 1224
 <212> DNA
 <213> Homo sapiens

<400> 35
 gcgcccctgg cctccagctg cgcaggagcc tgtggtacca gcttcccaga tggcctcacc 60
 cctgagggaa cccaggcctc cggggacaag gacattcctg caattaacca agggctcacc 120
 ctggaagaaa cccagagag cagcttccct atcgaggggg acatcatccg gccgagtcac 180
 ttccgactgc tgtcagcaac cagcaacaaa tggcccatgg gtggtagtgg tgcgtgggag 240
 gtccccttcc tgcctcccag caagtacgat gagcccagcc gccaggtcat cctcgaggct 300
 cttgaggagt ttgaacgttc caoigtgcac aggtttgtca cctatcagga ccagagagac 360
 ttcatttcca tcatccccc gtatgggtgc ttctcgagtg tggggcgagc tggaggagtg 420
 caggtgtgtc ccttgccgcc caoigtgttc cagaagggcc ggggcattgt ccttcagtag 480
 ctcagtcagt tgcctgggctt ctggcacagag cacacggcgg ccgacccgga ccgctatata 540
 cgtgtcaact ggaacgagat cctgccaggc ttgaaatca acttcatcaa cctcgaggag 600
 agcaacatgc tgaacgccta tgactactcc tctgtgatgc actatgggag gctcgccttc 660
 agccggcggt ggtgccccac catcacacca ctttggggcc ccagtgtcca catcgccagc 720
 cgatggaaac tgagtgccct ggacatcacc cgggtcctca aactctacgg ctgcagccca 780
 agtggcccac ggcccgtgg gagagggtcc catgccacca gcactggtag gaggcccgct 840
 cgggcctccc tatctctgca gcggcttttg gaggcactgt cggcggaatc caggagcccc 900
 gaccccgagt gttccagtg cggaggccag cccgttccct cagggcctgg ggagagccca 960

```

catgggtggg agtccccctgc cctgaaaaag ctcagtgacg aggcctcggc aaggcagcct 1020
cagaccctag cttcctcccc aagatcaagg cctggagcag gtgccccggg tgttgctcag 1080
gagcagtcct ggctggccgg agtgtccacc aagcccacag tcccattctt agaagcagga 1140
atccagccag tccctgtcca gggaagccca gctctgccag ggggtgtgtt acctagaaat 1200
catttcaagg ggaatgccga agat 1224

```

```

<210> 36
<211> 408
<212> PRT
<213> Homo sapiens

```

```

<400> 36
Ala Pro Leu Ala Ser Ser Cys Ala Gly Ala Cys Gly Thr Ser Phe Pro
1 5 10 15
Asp Gly Leu Thr Pro Glu Gly Thr Gln Ala Ser Gly Asp Lys Asp Ile
20 25 30
Pro Ala Ile Asn Gln Gly Leu Ile Leu Glu Glu Thr Pro Glu Ser Ser
35 40 45
Phe Leu Ile Glu Gly Asp Ile Ile Arg Pro Ser Pro Phe Arg Leu Leu
50 55 60
Ser Ala Thr Ser Asn Lys Trp Pro Met Gly Gly Ser Gly Val Val Glu
65 70 75 80
Val Pro Phe Leu Leu Ser Ser Lys Tyr Asp Glu Pro Ser Arg Gln Val
85 90 95
Ile Leu Glu Ala Leu Ala Glu Phe Glu Arg Ser Thr Cys Ile Arg Phe
100 105 110
Val Thr Tyr Gln Asp Gln Arg Asp Phe Ile Ser Ile Ile Pro Met Tyr
115 120 125
Gly Cys Phe Ser Ser Val Gly Arg Ser Gly Gly Met Gln Val Val Ser
130 135 140
Leu Ala Pro Thr Cys Leu Gln Lys Gly Arg Gly Ile Val Leu His Glu
145 150 155 160
Leu Met His Val Leu Gly Phe Trp His Glu His Thr Arg Ala Asp Arg
165 170 175
Asp Arg Tyr Ile Arg Val Asn Trp Asn Glu Ile Leu Pro Gly Phe Glu
180 185 190
Ile Asn Phe Ile Lys Ser Arg Ser Ser Asn Met Leu Thr Pro Tyr Asp
195 200 205
Tyr Ser Ser Val Met His Tyr Gly Arg Leu Ala Phe Ser Arg Arg Gly
210 215 220
Leu Pro Thr Ile Thr Pro Leu Trp Ala Pro Ser Val His Ile Gly Gln

```

225 230 235 240
 Arg Trp Asn Leu Ser Ala Ser Asp Ile Thr Arg Val Leu Lys Leu Tyr
 245 250 255
 Gly Cys Ser Pro Ser Gly Pro Arg Pro Arg Gly Arg Gly Ser His Ala
 260 265 270
 His Ser Thr Gly Arg Ser Pro Ala Pro Ala Ser Leu Ser Leu Gln Arg
 275 280 285
 Leu Leu Glu Ala Leu Ser Ala Glu Ser Arg Ser Pro Asp Pro Ser Gly
 290 295 300
 Ser Ser Ala Gly Gly Gln Pro Val Pro Ala Gly Pro Gly Glu Ser Pro
 305 310 315 320
 His Gly Trp Glu Ser Pro Ala Leu Lys Lys Leu Ser Ala Glu Ala Ser
 325 330 335
 Ala Arg Gln Pro Gln Thr Leu Ala Ser Ser Pro Arg Ser Arg Pro Gly
 340 345 350
 Ala Gly Ala Pro Gly Val Ala Gln Glu Gln Ser Trp Leu Ala Gly Val
 355 360 365
 Ser Thr Lys Pro Thr Val Pro Ser Ser Glu Ala Gly Ile Gln Pro Val
 370 375 380
 Pro Val Gln Gly Ser Pro Ala Leu Pro Gly Gly Cys Val Pro Arg Asn
 385 390 395 400
 His Phe Lys Gly Met Ser Glu Asp
 405
 <210> 37
 <211> 300
 <212> PRT
 <213> Homo sapiens
 <400> 37
 Met Leu Arg Leu Trp Asp Phe Asn Pro Gly Gly Ala Leu Ser Asp Leu
 1 5 10 15
 Ala Leu Gly Leu Arg Gly Met Glu Glu Gly Gly Tyr Ser Cys Ala Gly
 20 25 30
 Ala Cys Gly Thr Ser Phe Pro Asp Gly Leu Thr Pro Glu Gly Thr Gln
 35 40 45
 Ala Ser Gly Asp Lys Asp Ile Pro Ala Ile Asn Gln Gly Leu Ile Leu
 50 55 60
 Glu Glu Thr Pro Glu Ser Ser Phe Leu Ile Glu Gly Asp Ile Ile Arg
 65 70 75 80

```

Pro Ser Pro Phe Arg Leu Leu Ser Ala Thr Ser Asn Lys Trp Pro Met
      85                      90                      95
Gly Gly Ser Gly Val Val Glu Val Pro Phe Leu Leu Ser Ser Lys Tyr
      100                      105                      110
Asp Glu Pro Ser His Gln Val Ile Leu Glu Ala Leu Ala Glu Phe Glu
      115                      120                      125
Arg Ser Thr Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp Phe
      130                      135                      140
Ile Ser Ile Ile Pro Met Tyr Gly Cys Phe Ser Ser Val Gly Arg Ser
      145                      150                      155                      160
Gly Gly Met Gln Val Val Ser Leu Ala Pro Thr Cys Leu Gln Lys Gly
      165                      170                      175
Arg Gly Ile Val Leu His Glu Leu Met His Val Leu Gly Phe Trp His
      180                      185                      190
Glu His Thr Arg Ala Asp Arg Asp Arg Tyr Ile Arg Val Asn Trp Asn
      195                      200                      205
Glu Ile Leu Pro Gly Phe Glu Ile Asn Phe Ile Lys Ser Gln Ser Ser
      210                      215                      220
Asn Met Leu Thr Pro Tyr Asp Tyr Ser Ser Val Met His Tyr Gly Arg
      225                      230                      235                      240
Leu Ala Phe Ser Arg Arg Gly Leu Pro Thr Ile Thr Pro Leu Trp Ala
      245                      250                      255
Pro Ser Val His Ile Gly Gln Arg Trp Asn Leu Ser Ala Ser Asp Ile
      260                      265                      270
Thr Arg Val Leu Lys Leu Tyr Gly Cys Ser Pro Ser Gly Pro Arg Pro
      275                      280                      285
Arg Gly Arg Gly Glu Trp His Gly Arg Lys Val Thr
      290                      295                      300

```

```

<210> 38
<211> 5005
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> pCR4 TOPO IPAAA78836-1 plasmid sequence

```

```

<400> 38
acgcgcccaat acgcaaacgc cctctccccg cgcgttgccc gattcattaa tgcagctggc 60
acgacaggtt tccgactgg aaagcgggca gtgagcgcaa cgcaattaat gtgagttagc 120
tcactcatta ggcaccccag gctttacact ttatgcttcc ggctcgtatg ttgtgtggaa 180

```

ttgtgagcgg	ataacaattt	cacacaggaa	acagctatga	ccatgattac	gccaaagctca	210
gaattaaacc	tcaactaaagg	gaactagtcc	gcaggtttaa	acgaattccg	ccttagccac	300
aggcttaate	tccggacact	cccttgaaat	gattttctagg	tacacagccc	ccttgccagag	360
ctgggcttcc	ctggacaggg	actggctgga	ttcctgcttc	tgaagatggg	actgtgggct	420
gggtggacac	tccggccagg	caggactgct	cctgagcaac	accgggggga	cctgtcccaag	480
gccttgatct	tggggagqaa	gctagggtct	gaggtgcct	tggcagagcc	tttgcaactga	540
gctttttccg	caggagggac	tcaccaacat	gtgggtctct	cccagccgct	gcaggaacgg	600
gctggcctcc	gcacactggaa	ccactggggg	cggggctcct	ggattccgcg	gacagtgcct	660
ccaaaagccg	ctgcagagat	agggaggccg	ggggggggct	cctaccagtg	ctgtgggcat	720
gggacccctc	cccacggggc	ctggggccac	ttgggctgca	gcctgagatg	ttgaggaccc	780
gggtgatgct	cgaggcaact	aggttccatc	gctggccgat	gtggacactg	ggggcccaaa	840
gtgtgtgat	ggtgggcagg	ccacgcccgc	tgaaggcag	cctcccatag	tgcatacacg	900
aggagtagtc	ataggcgctc	agcatgttgc	tgctctgaga	cltgatgaag	ttgatttcaa	960
agcctggcag	gatctcgctc	cagttgacac	ggatatagcg	gtcccggctg	gcccgcgtgt	1020
gctcgtgcc	gaagcccagg	acatgcatag	gctcatgaag	gacaatgccc	cgggccctct	1080
ggagacaag	ggggcccgag	gagaccacct	gcactccctc	actgcgcccc	acactcgaga	1140
agcaccatac	catggggatg	atggaaatga	agtcctctct	gtcctgatag	tgacaaaaac	1200
tgatgcacgt	ggaaacttca	aactccgcaa	gagcctccag	gatgacatcg	cggtcgggct	1260
catcgtaact	gctggagagc	aggaaggggg	cctccacgac	accactacca	cccatggccc	1320
attttgtgct	ggttgcctgac	agaaggcgca	attccggccc	gctaaattca	attcgcccta	1380
tagtgagtgc	tattacaatt	cactggccgt	cggttttcaa	cgtcgtgact	gggaaaaacc	1440
tggcgttacc	caacttaate	gccttgccag	acatccccc	ttcgccagct	ggcgtaaatg	1500
cgaaagttcc	cgacccgcat	gccttccca	acagttggcg	atgcctatag	tacggcagtt	1560
taaggtttac	acctataaaa	gagagagccg	ttatcgtctg	tttgtggatg	tacagagtga	1620
tattattgac	acgcgggggc	cagcggatgt	gatccccctg	gccagtgcac	gtctgctgtc	1680
agataaaagc	tcccgtgaac	tttaccgggt	ggtgcacatc	ggggatgaaa	gctggcgcat	1740
gatgaccacc	gatalggcca	gtgtgcgggt	ctccgtttatc	gggggaagaag	tggctgatct	1800
cagccaccgc	gaaaaatgca	tcaaaaacgc	cattaaatgc	atgttctggg	gaatatataat	1860
gtcagggcat	agattttcaa	aaaggaatct	cacctagatc	cttttcaact	agaaaagccag	1920
tccgcagaaa	cggtgctgac	cccggaatga	tgtcagctac	tgggctatct	ggaccaaggga	1980
aaacgcagac	gcacaaagaa	agcaggtagc	ttgcagtggt	cttacaatgg	gatagctaga	2040
ctgggcgggt	ttatggacag	caagcgaaac	ggaattgcca	gctggggggc	cctctggtaa	2100
ggttgggaag	ccctgcaaa	taaaactggat	ggctttctcg	ccgccaagga	ttctgatggc	2160
caggggatca	agctctgctc	aagagacagg	atgaggatcg	tttcgatga	ttgaacaaga	2220
tggattgcac	gcaggttctc	cggccgcttg	ggtggagagg	ctattcggct	atgactgggc	2280
caacacagaa	atcggtgctc	ctgatgcgcg	cgtgttccgg	ctgtcagcgc	agggcgccgc	2340
ggttcttttt	gtcaagacgc	acctgtccgg	tgcctgaaat	gaactgcag	acgagcgacg	2400
ggggctatcg	tggctggcca	cgacggcggt	tccttgccga	gctgtgctcg	acgttgtcac	2460
tgaagcggga	agggactggc	tgtctattgg	cgaagtgcgc	gggcaggatc	tcctgtcacc	2520
tcaacttgct	cctgcggaga	aagtatccat	gcaattgcat	gcgaatgcgc	ggctgcatac	2580
gcttgatccg	gctacccgcc	catcgacca	ccaagcgaaa	catcgcatcg	agcagacacg	2640
tactcgatgc	gaagcgggtc	ttgtcgatca	ggatgatctg	gacgaagagc	atcaggggct	2700
cgccgcagcg	gaactgttgc	ccaggctcaa	ggcgagcatg	cccgcagcg	aggaatcctg	2760
cgtgaccact	ggcgatgcct	gcttgccgaa	tatcatgggt	gaaaaatggc	gcttttcttg	2820
attcatcgac	tgtggccggc	ggagccgatg	caggacatag	cgtctcctcg	tgcttgctac	2880
ccgtgatatt	ctgtgaagag	ttggccggga	atgggctgac	cgcttctcgc	tgttttaacg	2940
tatcgccgct	cccgatcgcg	agcgcatcgc	ctctcatcgc	ctctctgact	agcttctctg	3000
aattattaac	gcttacaatt	tcctgatcgc	gtattttctc	cttacgcact	tgtgcggatg	3060
ttcacaccgc	atacaggtgg	cacttttcgg	ggaaatgctg	gcgggaacccc	tttttgttta	3120
ttttttctaaa	tacattctaaa	tatgtatccg	ctcatgagac	aataaccctg	ataaatgctt	3180
caataaattt	gaaaaaggaa	agatatagat	attcaacatt	tcctgtgcgc	ccttatcccc	3240
ttttttcgcg	cattttgcct	tcctgttttt	ctcatccacc	aaacgcctgg	gaaagttaaaa	3300
gatgctgaag	atcagttggg	tgcacagtg	ggttacatcg	aactgcatct	caacagcggg	3360
aagatctctg	agagttggc	ccccgaagaa	cgttttccaa	tgatgagcac	tttttaagtt	3420
ctgctatgtg	gcgcgggtatt	atcccgattt	gacgcggggc	aagagcaact	cggtgcgcgc	3480

atacactatt	ctcagaatga	cttggttgag	tactcaccag	tcacagaaaa	gcactcttacg	3540
gatggcatga	cagtaagaga	attatgcagt	gctgccataa	ccatgagtgga	taacactgcg	3600
gccaaacttac	ttctgcacaac	gatcggagga	cgaaggagc	taaccgcctt	tttgacacaac	3660
atgggggagc	atgtaactgc	ccttgatcgt	tgggaaccgg	agctgaatga	agccataacca	3720
aacgcagcagc	gtgacacacac	gatgcctgta	gcaatggcaa	caacggttcg	caaaactatta	3780
actggcggaac	tacttactct	agcttcccg	caacaattaa	tagactggat	ggaggcggaat	3840
aaagtgtcag	gacaaactct	gcgctcgcc	cttcggctg	gctgggttat	tgctgataaa	3900
cttgagcagc	gtgagcgtgg	gtctcgcggt	atcattgcag	cactggggcc	agatgggtaag	3960
ccctcccgta	tctgagttag	ctacacgacg	gggagtcagg	caactatgga	tgaacgaaat	4020
agacagatgc	ctgagatagg	tgccctcactg	atlaagcatt	ggtaactgtc	agaccaaggt	4080
tactcatata	tacttttagat	tgattttaaaa	cttcattttt	aattttaaag	gatctaggtg	4140
aaagatccctt	ttgataaatct	catgacacaaa	atcccttaac	gtgagtttct	gttccactga	4200
gcgtcagacc	ccgtagaaaa	gatcaaaagga	tcttcttgag	atcccttttt	tctgcgcgta	4260
atctgctgct	tgcaaaacaaa	aaaaccaccg	ctacacgcgg	tgggtttgtt	gocggatcaa	4320
gcttaccocaa	ctcttttttcc	gaaggttaact	ggcttcagca	gagcgcagat	accaaataact	4380
gtccttctag	tgtagccgta	gtlaggccac	cacttcaaga	actctgtagc	accgcctaca	4440
tacctcgtct	tgtctaactct	gttaccagtg	gctgctgcc	gtggcgataa	gtcgtgtctt	4500
accgggttgg	actcaagacg	atagttaccg	gataaggcgc	agcggctcgg	ctgcaacggg	4560
ggttcgtgca	cacagcccg	cttgagcgca	acgacctaca	cgaactgagc	gtacctacag	4620
cgttgagctat	gagaaagcgc	cacgcttccc	gaaggagaaa	agggcgacag	atatccggtt	4680
agcggcaggg	toggaaacag	agagcgcacg	agggagcttc	cagggggaaa	cgctcgtgat	4740
ctttatagtc	ctgtcgggtt	tgcgcacctc	tgaactgagc	gtcgtatttt	gtgagctcgc	4800
tcaggggggc	ggagcctatg	gaaaaaacgc	agcaaacgcg	cttctttacg	gttccctgac	4860
ttttgtcggc	cttttgcctc	catgttcttt	cctgcgttat	ccctgattc	tgtgggataac	4920
cgtattaccg	cctttgagtg	agctgatacc	gctcgcgcga	gccgaacgac	cagcgcgcgc	4980
gagtcagtg	gcgaggaagc	ggaag				5005

<210> 39
 <211> 5269
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> XpCR4TOPO IPAA78836-2 plasmid sequence

<400> 39						
agcgcccaat	acgcaaacgc	ctctctcccg	cgcgttggcc	gattcattaa	tgcagctggc	60
acgaacaggt	tccgcactcg	aaagcgggca	gtgagcgcaa	cgcaattaat	gtgagttagc	120
tcactcatta	ggcaccgcc	gctttacact	ttatgcttcc	ggctcgtatg	ttgtgtggaa	180
tgttgagcgg	ataacaattt	caacacaggaa	acagctatga	ccatgattac	gccaaagctca	240
gaattaaacc	tcactaaagg	gactagtcct	gcaggtttaa	acgaattcgc	ccttagccac	300
aggtcttaac	ttcggacatc	cccttgaatt	gatttctagg	tacacagccc	cctgcagagc	360
ctgggcttcc	ctcgacaggc	actggctgga	tctcgtcttc	tgaagatggg	actgtgggct	420
tgttggaacc	tccggccagc	caggactgct	cctgagcaac	accgggggca	ctctgccag	480
gccttgatct	tggggaggaa	gctaggggtc	gaggctgcct	tgccgagggc	tctgcactga	540
gcttttttcc	ggcaggggac	tcccaaccat	gtgggctctc	cccaggccct	gcaggaaacg	600
gctggctctc	cgcaactggaa	ccactggggt	cggggctcct	ggacttcggc	gacagctgc	660
ccaaagccg	ctcgacagat	agggaggccg	gagcgggctc	cctaccagtg	ctbtggggat	720
gggacccctc	ccacgcgggc	ctggggccac	ttgggctgca	ccgctagagt	ttgagacccc	780
gggtgatgtc	cgaggcactc	aggttccatc	gctggccgat	gtggacactg	ggggcccaaa	840
gtggtgtgat	ggtgggcagc	ccacgcgggc	tgaaggcgag	cctcccatag	tgcatacacg	900
aggagtagtc	ataggcgctc	agcatgttgc	cttgccgaga	cttgatgaag	ttgatttcaa	960
agcctggcag	gatctcgttc	cagttgacac	ggatatagcg	gtcccggtcg	gccccggtgt	1020
gctcgtgcca	gaagccagc	acatgcatga	gctcatgaag	gacaaatgcc	cggccctctc	1080
ggagacacgt	ggggcgccag	gagaccacct	gcactccctc	actgcgcccc	acactcgaga	1140

agcaccata	catggggatg	atggaaatga	agtctctctg	gtctctgatg	gtgacaaacc	1200
tgatgcacgt	ggaaacgttca	aactccgcaa	gagcctccag	gatgacctcg	cggctgggct	1260
catcgtactt	gctggagagc	aggaagggga	cctccacgac	accactacca	cccatggggc	1320
attttgttget	ggttgctgac	agcagtcgga	agggactcgg	ccggatgatg	tccccctcga	1380
tgaggaaagt	gctctctcggg	gtttcttcca	ggatgagccc	ttggttaatt	gcaggaaatgt	1440
ccttgtcccc	ggaggcctgg	gttccctcag	gggtgagggc	atctgggaag	ctggaccac	1500
aggctcctgc	gcagctgcag	gccaggggcg	ctctcaggat	cacacctcgg	aaggagagca	1560
gaccaccgac	ccaaggccag	agaccoccta	caacctccat	ggtagaaagg	gcgaattcgc	1620
ggcgcctaaa	ttcaattcgc	cctatagtga	gtcgtattac	aattcactgg	ccgttgtttt	1680
acaacgtcgt	gactgggaaa	acctcggcgt	tacccaactt	aatcgcttg	cagcacatcc	1740
ccctttcgcc	agctggcgta	atagcgaaga	ggccgcgacc	gatcgccctt	cccaacagtt	1800
cgcgaccta	tacgtacggc	agtttaagggt	ttacacctat	aaaagagaga	gcccgttatcg	1860
ctctgtttgtg	gatgtacaga	gtgatattat	tgacacggcg	ggcgacgga	tgggtatccc	1920
cctggccagt	gcacgtctgc	tgtcagataa	agttctccgl	gaactttacc	cgggtgtgca	1980
tatcggggat	gaaagctggc	gcctgatgac	cacogatatg	gccagtgtgc	cggctctccgt	2040
tatcggggaa	gaagtggctg	atctcagcca	cgcggaataa	gacatcaaaa	acgccattaa	2100
ccctgatttc	tggggaaatc	aaatgtcagg	catgagatta	tcaaaaagga	tcttccacct	2160
gatccttttc	acgtgaaaag	ccagtcgcga	gaaacggtgc	tgaccctcga	tgaaatgcag	2220
ctaactgggt	atctcggcaa	gggaaaacgc	aagcgcaagg	agaaaagcag	tagcttgcag	2280
tgggcttaaca	tggcgctggc	tagactgggc	gggttttatg	acagcaagcg	aaccggaatt	2340
gccacgtggg	ggcgcctctg	gtaagggttg	gaagccctcg	aaagttaact	ggatggcttt	2400
ctcgcccgca	aggatctgat	ggcgccgggg	atcaagctct	gatcaagaga	caggatggag	2460
atcgctttcgc	atgattgaac	aaagatggatt	gcacgcaggt	cttcggcgcg	cttgggtgga	2520
gaggctattc	ggctatgact	gggcacaaca	gacaactcgg	tgtctctgat	cgcgcgtgtt	2580
ccggctgtca	gcgcaggggc	gcccggttct	ttttgtcaag	accgactcgt	cgcgtgccct	2640
gaatgaactg	caagacgagg	cagcgcggt	atcgtggctg	gccacgacg	gcgttccctg	2700
cgcagctgtg	ctcgacgttg	tcaactgaagc	gggaaggggc	tggtcgtcat	tggggcgaat	2760
gccggggcag	gattctcgtg	catctcaact	tgtcctcgcc	gagaaagtat	ccatcactgc	2820
tgatgcaatg	cggcgctcgc	atacgcttga	tccggctacc	tgccacttcg	accaccaagc	2880
gaaacactgc	atcgacgtga	caacglactcg	gatggaagcg	ggtcttctgc	atcaggatga	2940
ctctgacgaa	gagcatcagg	ggctcgcgcc	agccgaaactg	ttcgccaggc	tcaaggcgag	3000
catgccccgc	ggcgaggatc	tgtctgtgac	ccatggcgat	gcctgcttgc	cgaatatcat	3060
ggtggaaaat	ggcgcgtttt	ctggattcat	cgaactgtgc	cggctgggtg	tggcgagcgc	3120
ctatcaggac	atagcgttgg	ctacccgtga	tatttgcgtga	gagcttggcg	gcgaattggcg	3180
tgaccgcttc	ctcgtgcttt	acgggtatgc	cgtcccgat	tcgcagcgca	tcgccttcta	3240
tcgccttttc	gacgagtctt	tctgaattat	taacgcttac	aatttctctga	tggcggttaa	3300
tctccttaag	catctgtgcg	gtattttaca	cgcgatacag	gtggcactgc	tcggggaaat	3360
gtgcgcggaa	ccctattttg	tttatttttc	taaatacatt	caaatatgta	tccgctcatg	3420
agacaaatac	ccctgataaat	gcttccaataa	tattgaaaaa	ggaagagtat	gagtatccaa	3480
catttccgtg	tcgcctttat	tccctttttt	goggcatttt	gccttctcgt	ttttgctcac	3540
ccagaaacgc	tgttgaaagt	aaaagatgct	gaagatcagt	tgggtgcacg	agtggtgtac	3600
atcgactcgc	atctcaacag	cgtgaagatc	cttgagagtt	ttcgccccga	agaaagctttt	3660
ccaatgatga	gcacttttaa	agttctgcta	tgtggcgcg	tattatcccg	tattgacgcc	3720
gggcaagagc	aacccggtgc	cgcgatacac	tattctcaga	atgaacttgt	tgagtaactca	3780
cngtcacag	aaaagcatct	tacggatggc	atgacagtaa	gagaaattatg	cagctgctgc	3840
ataaccatga	gtgataaacat	tgcggccaac	ttactcttga	caacgatcgg	aggaaccgaag	3900
gagctaaacg	cttttttgca	caacatgggg	gatactgtaa	ctcgccttga	tgttggtgaa	3960
ccggagactg	atgaagccat	acccaacgac	gagcgtgaca	ccacgatgcc	tgtgagcaatg	4020
gcaacaacgt	tgcgcacaact	attaaactggc	gaactactta	ctctagcttc	ccggcaacaa	4080
ttaatagact	ggatggaggc	ggataaagtt	gcaggaccac	ttctgcgcct	ggcccttcgc	4140
ctgggctcgt	tatttgcgtg	taaatctgga	gcgggtgtag	gtgggtctcg	cggtatcatt	4200
gcagcactgg	ggccagatgg	taagccctcc	cgtatcgtag	ttatctacac	gacggggagt	4260
caggcaacta	tggatgaacg	aaatagacag	atcgctgaga	taggctcctc	actgatgtaa	4320
cattgggtaac	tgtcagacca	agttttactca	tatatacttt	agatgttttt	aaaactccat	4380
ttttaattta	aaaggatcta	ggtgaagatc	ctttttgata	atctcatgac	caaaatccct	4440

```

taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa aggatcttct 4500
tgagatccct tttttctgcg cgtaatctgc tgccttgcaa caaaaaaacc accgctacca 4560
gcggttgllt gtttgccgga tcaagagcta ccaactcttt tlcggaaggt aactggcttc 4620
agcagagcgc agataccaaa tactgtccct ctagtgtagc cgtagttagg ccaccacttc 4680
aagaactctg tagcacccgc tacataccct gctctgctaa tctctgtacc agtggctgct 4740
gccagtgccg ataagtcgtg tcttacccgg ttggaactca gacgatagtt accggataag 4800
gcgcagcggt cgggctgaac ggggggttcg tgcacacagc ccagcttgga gcgaacgacc 4860
tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct tccogaaggg 4920
agaaagccgg acaggtatcc ggtaagccgc agggctcgaa caggagagcg cacgagggag 4980
cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca cctctgactt 5040
gagcgtcgat ttttgtgatg ctgctcaggg gggcggagcc tatggaaaaa cgccagcaac 5100
gcggcctttt tacggttctc gggcttttgc tggccttttg ctacacatgtt ctttctcgcg 5160
ttatccctcg attctgtgga taaccgtatt accgcctttg agtgagctga taccgctcgc 5220
cgcagccgaa cgaccgagcg cagcagagta gtgagcgagg aagcggag 5269

```

```

<210> 40
<211> 19
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Primer CP1

```

```

<400> 40
accgctatat cgtgtgcaa 19

```

```

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Primer CP2

```

```

<400> 41
gctgcagccg tagagttt 18

```

```

<210> 42
<211> 25
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> GeneRacer 3' Primer

```

```

<400> 42
gctgtcaacg atacgctacg taacg 25

```

```

<210> 43
<211> 26
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> 78836-GR1-3' Primer

```

```

<400> 43
agtggtccaca tcggccagcg atggaa      26

<210> 44
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> GeneRacer 3' nested primer

<400> 44
cgctacgtaa cggcatgaca gtg          23

<210> 45
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> 78836-GRlnest-3' primer

<400> 45
atggaacctg agtgcctcgg acatc      25

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> 78836-FL-F primer

<400> 46
ctgtcagcaa ccagcaacaa          20

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> 78836-FL-R primer

<400> 47
agccacaggc ttaatcttcg          20

<210> 48
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> 78836-FL2-F primer

```

```

<400> 46
tctaccatgg aggggtgtagg 20

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> T3 primer

<400> 49
attaaccctc actaaaggga 20

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> T7 primer

<400> 50
taatacgaact cactataggg 20

<210> 51
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> SP6 primer

<400> 51
atttaggtga cactatag 18

<210> 52
<211> 230
<212> PRT
<213> Homo Sapiens

<400> 52

Asp Lys Asp Ile Pro Ala Ile Asn Gln Gly Leu Ile Leu Glu Glu Thr
1 5 10 15
Pro Glu Ser Ser Phe Leu Ile Glu Gly Asp Ile Ile Arg Pro Ser Pro
20 25 30
Phe Arg Leu Leu Ser Ala Thr Ser Asn Lys Trp Pro Met Gly Gly Ser
35 40 45
Gly Val Val Glu Val Pro Phe Leu Leu Ser Ser Lys Tyr Asp Glu Pro

```

50 55 60
 Ser His Gln Val Ile Leu Glu Ala Leu Ala Glu Phe Glu Arg Ser Thr
 65 70 75 80
 Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp Phe Ile Ser Ile
 85 90 95
 Ile Pro Met Tyr Gly Cys Phe Ser Ser Val Gly Arg Ser Gly Gly Met
 100 105 110
 Gln Val Val Ser Leu Ala Pro Thr Cys Leu Gln Lys Gly Arg Gly Ile
 115 120 125
 Val Leu His Glu Leu Met His Val Leu Gly Phe Trp His Glu His Thr
 130 135 140
 Arg Ala Asp Arg Asp Arg Tyr Ile Arg Val Asn Trp Asn Glu Ile Leu
 145 150 155 160
 Pro Gly Phe Glu Ile Asn Phe Ile Lys Ser Gln Ser Ser Asn Met Leu
 165 170 175
 Thr Pro Tyr Asp Tyr Ser Ser Val Met His Tyr Gly Arg Leu Ala Phe
 180 185 190
 Ser Arg Arg Gly Leu Pro Thr Ile Thr Pro Leu Trp Ala Pro Ser Val
 195 200 205
 His Ile Gly Gln Arg Trp Asn Leu Ser Ala Ser Asp Ile Thr Arg Val
 210 215 220
 Leu Lys Leu Tyr Gly Cys
 225 230

 <210> 53
 <211> 231
 <212> PRT
 <213> Anguilla japonica

 <400> 53

 Asp Pro Asp Asp Val Asp Ile Thr Thr Ser Ile Leu Gln Ser Asn Asn
 1 5 10 15
 Gly Ser Ser Glu Ile Leu Met Glu Gly Asp Leu Ile Val Ser Asn Thr
 20 25 30
 Arg Asn Ala Met Lys Cys Trp Asn Asn Gln Cys Leu Trp Arg Lys Ser
 35 40 45
 Ser Asp Gly Leu Val Glu Val Pro Tyr Thr Val Ser Asn Glu Phe Ser
 50 55 60

```

Tyr Tyr His Lys Lys Arg Ile Glu Asn Ala Met Lys Thr Phe Asn Thr
65          70          75          80

Glu Thr Cys Ile Arg Phe Val Pro Arg Ser Ser Gln Arg Asp Phe Ile
85          90          95

Ser Ile Glu Ser Arg Asp Gly Cys Tyr Ser Tyr Leu Gly Arg Thr Gly
100         105         110

Gly Lys Gln Val Val Ser Leu Ala Arg Tyr Gly Cys Val Tyr His Gly
115         120         125

Ile Ile Gln His Glu Leu Asn His Ala Leu Gly Phe Tyr His Glu His
130         135         140

Thr Arg Ser Asp Arg Asp Glu Tyr Val Lys Ile Asn Trp Glu Asn Val
145         150         155         160

Ala Pro His Thr Ile Tyr Asn Phe Gln Thr Gln Asp Thr Asn Asn Leu
165         170         175

Asn Thr Pro Tyr Asp Tyr Thr Ser Ile Met His Tyr Gly Arg Thr Ala
180         185         190

Phe Ser Thr Asn Gly Met Asp Thr Ile Thr Pro Val Pro Asn Pro Asn
195         200         205

Gln Ser Ile Gly Gln Arg Arg Ser Met Ser Arg Gly Asp Ile Leu Arg
210         215         220

Ile Lys Lys Leu Tyr Ser Cys
225         230

```

```

<210> 54
<211> 86
<212> FRT
<213> Homo Sapiens

```

```

<400> 54

```

```

Ser Cys Ala Gly Ala Cys Gly Thr Ser Phe Pro Asp Gly Leu Thr Pro
1          5          10         15

Glu Gly Thr Gln Ala Ser Gly Asp Lys Asp Ile Pro Ala Ile Asn Gln
20         25         30

Gly Leu Ile Leu Glu Glu Thr Pro Glu Ser Ser Phe Leu Ile Glu Gly
35         40         45

Asp Ile Ile Arg Pro Ser Pro Phe Arg Leu Leu Ser Ala Thr Ser Asn
50         55         60

Lys Trp Pro Met Gly Gly Ser Gly Val Val Glu Val Pro Phe Leu Leu
65         70         75         80

```

Ser Ser Lys Tyr Asp Glu
85

<210> 55
<211> 86
<212> PRT
<213> Homo Sapiens

<400> 55

Ser Cys Ala Gly Ala Cys Gly Thr Ser Phe Pro Asp Gly Leu Thr Pro
1 5 10 15

Glu Gly Thr Gln Ala Ser Gly Asp Lys Asp Ile Pro Ala Ile Asn Gln
20 25 30

Gly Leu Ile Leu Glu Glu Thr Pro Glu Ser Ser Phe Leu Ile Glu Gly
35 40 45

Asp Ile Ile Arg Pro Ser Pro Phe Arg Leu Leu Ser Ala Thr Ser Asn
50 55 60

Lys Trp Pro Met Gly Gly Ser Gly Val Val Glu Val Pro Phe Leu Leu
65 70 75 80

Ser Ser Lys Tyr Gly Glu
85

<210> 56
<211> 1103
<212> DNA
<213> Homo Sapiens

<220>
<221> exon
<222> {101}..(1000)

<400> 56

agggtccttgt ggacaatagc tattottottt ggcctgtgtcg cttcccttca ctgggtgcag 60

gtgactgtgg ggggtgtccc aaatgctgcc cagcgtgtgac atg ctc cgc ctc tgg 115
Met Leu Arg Leu Trp
1 5

gat ttc aat cca ggt ggg gcc ctg agt gac ctg gct ctg ggg ctc agg 163
Asp Phe Asn Pro Gly Gly Ala Leu Ser Asp Leu Ala Leu Gly Leu Arg
10 15 20

ggg atg gag gag ggg gga tat agc tgc gca gga gcc tgt ggt acc agc 211
Gly Met Glu Glu Gly Gly Tyr Ser Cys Ala Gly Ala Cys Gly Thr Ser
25 30 35

ttc cca gat ggc ctc acc cct gag gga acc cag gcc tcc ggg gac aag Phe Pro Asp Gly Leu Thr Pro Glu Gly Thr Gln Ala Ser Gly Asp Lys 40 45 50	259
gac att cct gca att aac caa ggg ctc atc ctg gaa gaa acc cca gag Asp Ile Pro Ala Ile Asn Gln Gly Leu Ile Leu Glu Glu Thr Pro Glu 55 60 65	307
agc agc ttc ctc atc gag ggg gac atc atc cgg ccg agt ccc ttc cga Ser Ser Phe Leu Ile Glu Gly Asp Ile Ile Arg Pro Ser Pro Phe Arg 70 75 80 85	355
ctg ctg tca gca acc agc aac aaa tgg ccc atg ggt ggt agt ggt gtc Leu Leu Ser Ala Thr Ser Asn Lys Trp Pro Met Gly Gly Ser Gly Val 90 95 100	403
gtg gag gtc ccc ttc ctg ctc tcc agc aag tac gat gag ccc agc cat Val Glu Val Pro Phe Leu Leu Ser Ser Lys Tyr Asp Glu Pro Ser His 105 110 115	451
cag gtc atc ctg gag gct ctt gcg gag ttt gaa cgt tcc acg tgc atc Gln Val Ile Leu Glu Ala Leu Glu Phe Glu Arg Ser Thr Cys Ile 120 125 130	499
agg ttt gtc acc tat cag gac cag aga gac ttc att tcc atc atc ccc Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp Phe Ile Ser Ile Ile Pro 135 140 145	547
atg tat ggg tgc ttc tcg agt gtg ggg cgc agt gga ggg atg cag gtg Met Tyr Gly Cys Phe Ser Ser Val Gly Arg Ser Gly Gly Met Gln Val 150 155 160 165	595
gtc tcc ctg gcg ccc acg tgt ctc cag aag ggc ccg ggc att gtc ctt Val Ser Leu Ala Pro Thr Cys Leu Gln Lys Gly Arg Gly Ile Val Leu 170 175 180	643
cat gag ctc atg cat gtg ctg ggc ttc tgg cac gag cac acg cgg gcc His Glu Leu Met His Val Leu Gly Phe Trp His Glu His Thr Arg Ala 185 190 195	691
gac cgg gac cgc tat atc cgt gtc aac tgg aac gag atc ctg cca ggc Asp Arg Asp Arg Tyr Ile Arg Val Asn Trp Asn Glu Ile Leu Pro Gly 200 205 210	739
tll gaa atc aac ttc atc aag tct cag agc agc aac atg ctg acg ccc Phe Glu Ile Asn Phe Ile Lys Ser Gln Ser Ser Asn Met Leu Thr Pro 215 220 225	787
tat gac tac tcc tct gtg atg cac tat ggg agg ctc gcc ttc agc cgg Tyr Asp Tyr Ser Ser Val Met His Tyr Gly Arg Leu Ala Phe Ser Arg 230 235 240 245	835
cgt ggg ctg ccc acc atc aca cca ctt tgg gcc ccc agt gtc cac atc Arg Gly Leu Pro Thr Ile Thr Pro Leu Trp Ala Pro Ser Val His Ile	883

250	255	260	
ggc cag cga tgg aac ctg agt gcc tcg gac atc acc cgg gtc ctc aaa			931
Gly Gln Arg Trp Asn Leu Ser Ala Ser Asp Ile Thr Arg Val Leu Lys			
265	270	275	
ctc tac ggc tgc agc cca agt ggc ccc agg ccc cgt ggg aga ggt gag			979
Leu Tyr Gly Cys Ser Pro Ser Gly Pro Arg Pro Arg Gly Arg Gly Glu			
280	285	290	
tgg cat ggc agg aag gtg act tgaacctgga gaaggcgccgt gtgctctaatt			1030
Trp His Gly Arg Lys Val Thr			
295	300		
ggtgtcaggg aggggtgacaa ggaggagat gaggttcag ggggagcagg gtgagatcac			1090
gggggcttgc cac			1103
<210> 57			
<211> 1554			
<212> DNA			
<213> Homo Sapiens			
<220>			
<221> exon			
<222> {2}..{502}			
<400> 57			
a tgg aac ctg agt gcc tcg gac atc acc cgg gtc ctc aaa ctc tac ggc			49
Trp Asn Leu Ser Ala Ser Asp Ile Thr Arg Val Leu Lys Leu Tyr Gly			
1 5 10 15			
tgc agc cca agt gcc ccc agg ccc cgt ggg aga ggg tcc cat gcc cac			97
Cys Ser Pro Ser Gly Pro Arg Pro Arg Gly Arg Gly Ser His Ala His			
20 25 30			
agc act ggt agg agc ccc gct ccg gcc tcc cta tct ctg cag cgg ott			145
Ser Thr Gly Arg Ser Pro Ala Pro Ala Ser Leu Ser Leu Gln Arg Leu			
35 40 45			
ttg gag gca ctg tcg gcg gaa tcc agg agc ccc gac ccc agt ggt tcc			193
Leu Glu Ala Leu Ser Ala Glu Ser Arg Ser Pro Asp Pro Ser Gly Ser			
50 55 60			
agt gcg gga ggc cag ccc gtt cct gca ggg cct ggg gag agc cca cat			241
Ser Ala Gly Gly Gln Pro Val Pro Ala Gly Pro Gly Glu Ser Pro His			
65 70 75 80			
ggg tgg gag tcc cct gcc ctg aaa aag ctc agt gca gag gcc tcg gca			289
Gly Trp Glu Ser Pro Ala Leu Lys Lys Leu Ser Ala Glu Ala Ser Ala			
85 90 95			
agg cag cct cag acc cta gct tcc tcc cca aga tca agg cct gga gca			337

Arg Gln Pro Gln Thr Leu Ala Ser Ser Pro Arg Ser Arg Pro Gly Ala	
100 105 110	
ggg gcc ccc ggt gtt gct cag gag cag tcc tgg ctg gcc gga gtg tcc	385
Gly Ala Pro Gly Val Ala Gln Glu Gln Ser Trp Leu Ala Gly Val Ser	
115 120 125	
acc aag ccc aca gtc cca tct tca gaa gca gga atc cag cca gtc cct	433
Thr Lys Pro Thr Val Pro Ser Ser Glu Ala Gly Ile Gln Pro Val Pro	
130 135 140	
gtc cag gga agc cca gct ctg cca ggg ggc tgt gta cct aga aat cat	481
Val Gln Gly Ser Pro Ala Leu Pro Gly Cys Val Pro Arg Asn His	
145 150 155 160	
ttc aag ggg atg tcc gaa gat taagcctgtg gcttctgtcc ccaagtaggg	532
Phe Lys Gly Met Ser Glu Asp	
165	
agggcatcct ctgccacgtg gagctgggtc gtctacctct tggctccttt gggccacacc	592
actgtcttcc agccccaacc taccaacca tctcagaggg ccaggactct tccctgtct	652
ctcttcaactg tgttccccta agggctccta gggccagggg ttcttctagc tctgccacag	712
gggaaggcag gcttggtgtg gctgtctctt gacttttgcc cagccctggt ggatgctggg	772
aalgggaggt gacattctcc agggacaggt cctggaaggg gtggggaaga ggtaggttcc	832
agccccgcag aaccctggaa tccctcctgt gctgaggcc ctgccccca gcatggaacta	892
atgggtgtcc taactctccc tcagggcagc cctgtggtgt ggaccctggg aacagcctcc	952
catccccccc aacatgcccc agtgtggggg aatgttctac agcagtgtga cctccagccc	1012
ttctctccag gaggtcttga gagcccaact taactccctg cagagcagga aggtggtagg	1072
tcaagtgtgg ccaccatttg ggagacgaga aagaagtggg gccccaccag attgcacaat	1132
gggaacotca gctggccctt gaacagagga ctacgttgtc tccacctac accgtatttc	1192
cctggagctc agccaggcgc agccttgaa ggagaaaggg ctgggggttac ctggcttgtc	1252
ctctccagg aaagcccctt tctctctctg cccagctcc cagcctggcc tctccaggc	1312
aggccctact cctctgcccc agctccggct ttccccatga ggtttgtccc aggcataag	1372
aaagcatcca ggggtccaat gagtgggcct agggcagagg ccctcagtc ccaagggtta	1432
ctgttttggg ggccttccag agggccaagg aagccctgct tggggtagaa ggggcaggag	1492
ccccacatgt tgggggagga aataaagtgg agtgtgtgtg gctgaaaaaa aaaaaaaaaa	1552
aa	1554

<210> 58
 <211> 1048
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> exon
 <222> (28)..(1035)

<400> 58
 ctgtcagcaa ccagcaacaa atggccc atg ggt ggt agt ggt gtc gtg gag gtc 54
 Met Gly Gly Ser Gly Val Val Glu Val
 1 5

ccc ttc ctg ctc tcc agc aag tac gat gag ccc agc cgc cag gtc atc 102
 Pro Phe Leu Leu Ser Ser Lys Tyr Asp Glu Pro Ser Arg Gln Val Ile
 10 15 20 25

ctg gag gct ctt gcg gag ttt gaa cgt tcc acg tgc atc agg ttt gtc 150
 Leu Glu Ala Leu Ala Glu Phe Glu Arg Ser Thr Cys Ile Arg Phe Val
 30 35 40

acc tat cag gac cag aga gac ttc att tcc atc atc ccc atg tat ggg 198
 Thr Tyr Gln Asp Gln Arg Asp Phe Ile Ser Ile Ile Pro Met Tyr Gly
 45 50 55

tgc ttc tcg agt gtg ggg cgc agt gga ggg atg cag gtg gtc tcc ctg 246
 Cys Phe Ser Ser Val Gly Arg Ser Gly Gly Met Gln Val Val Ser Leu
 60 65 70

gcg ccc acg tgt ctc cag aag gcc cgg gcc att gtc ctt cat gag ctc 294
 Ala Pro Thr Cys Leu Gln Lys Gly Arg Gly Ile Val Leu His Glu Leu
 75 80 85

atg cat gtg ctg gcc ttc tgg cac gag cac acg cgg gcc gac cgg gac 342
 Met His Val Leu Gly Phe Trp His Glu His Thr Arg Ala Asp Arg Asp
 90 95 100 105

cgc tat atc cgt gtc aac tgg aac gag atc ctg cca gcc ttt gaa atc 390
 Arg Tyr Ile Arg Val Asn Trp Asn Glu Ile Leu Pro Gly Phe Glu Ile
 110 115 120

aac ttc atc aag tct cag agc agc aac atg ctg acg ccc tat gac tac 438
 Asn Phe Ile Lys Ser Gln Ser Ser Asn Met Leu Thr Pro Tyr Asp Tyr
 125 130 135

tcc tct gtg atg cac tat ggg agg ctc gcc ttc agc cgg cgt ggg ctg 486
 Ser Ser Val Met His Tyr Gly Arg Leu Ala Phe Ser Arg Arg Gly Leu
 140 145 150

ccc acc atc aca cca ctt tgg gcc ccc agt gtc cac atc gcc cag cga 534
 Pro Thr Ile Thr Pro Leu Trp Ala Pro Ser Val His Ile Gly Gln Arg
 155 160 165

tgg aac ctg agt gcc tcg gac atc acc cgg gtc ctc aaa ctc tac ggc 582
 Trp Asn Leu Ser Ala Ser Asp Ile Thr Arg Val Leu Lys Leu Tyr Gly
 170 175 180 185

tgc agc cca agt ggc ccc agg ccc cgt ggg aga ggg tcc cat gcc cac 630
 Cys Ser Pro Ser Gly Pro Arg Pro Arg Gly Arg Gly Ser His Ala His
 190 195 200

agc act ggt agg agc ccc gcc ccg gcc tcc cta tct ctg cag cgg ett 678
 Ser Thr Gly Arg Ser Pro Ala Pro Ala Ser Leu Ser Leu Gln Arg Leu
 205 210 215

ttg gag gca ctg tcg gcg gaa tcc agg agc ccc gac ccc agt ggt tcc 726
 Leu Glu Ala Leu Ser Ala Glu Ser Arg Ser Pro Asp Pro Ser Gly Ser
 220 225 230

agt gcg gga ggc cag ccc gtt cct gca ggg cct ggg gag agc cca cat 774
 Ser Ala Gly Gly Gln Pro Val Pro Ala Gly Pro Gly Glu Ser Pro His
 235 240 245

ggg tgg gag tcc cct gcc ctg aaa aag ctc agt gca gag gcc tcg gca 822
 Gly Trp Glu Ser Pro Ala Leu Lys Lys Leu Ser Ala Glu Ala Ser Ala
 250 255 260 265

agg cag cct cag acc cta gct tcc tcc cca aga tca agg cct gga gca 870
 Arg Gln Pro Gln Thr Leu Ala Ser Ser Pro Arg Ser Arg Pro Gly Ala
 270 275 280

ggt gcc ccc ggt gtt gct cag gag cag tcc tgg ctg gcc gga gtg tcc 918
 Gly Ala Pro Gly Val Ala Gln Glu Gln Ser Trp Leu Ala Gly Val Ser
 285 290 295

acc aag ccc aca gtc cca tct tca gaa gca gga atc cag cca gtc cct 966
 Thr Lys Pro Thr Val Pro Ser Ser Glu Ala Gly Ile Gln Pro Val Pro
 300 305 310

gtc cag gga agc cca gct ctg cca ggg ggc tgt gta cct aga aat cat 1014
 Val Gln Gly Ser Pro Ala Leu Pro Gly Gly Cys Val Pro Arg Asn His
 315 320 325

ttc aag ggg atg tcc gaa gat taagcctgtg gct 1048
 Phe Lys Gly Met Ser Glu Asp
 330 335

<210> 59
 <211> 182
 <212> PRT
 <213> Homo Sapiens

<400> 59

Gly Val Val Glu Val Pro Phe Leu Leu Ser Ser Lys Tyr Asp Glu Pro
 1 5 10 15

Ser Arg Gln Val Ile Leu Glu Ala Leu Ala Glu Phe Glu Arg Ser Thr
 20 25 30
 Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp Phe Ile Ser Ile
 35 40 45
 Ile Pro Met Tyr Gly Cys Phe Ser Ser Val Gly Arg Ser Gly Gly Met
 50 55 60
 Gln Val Val Ser Leu Ala Pro Thr Cys Leu Gln Lys Gly Arg Gly Ile
 65 70 75 80
 Val Leu His Glu Leu Met His Val Leu Gly Phe Trp His Glu His Thr
 85 90 95
 Arg Ala Asp Arg Asp Arg Tyr Ile Arg Val Asn Trp Asn Glu Ile Leu
 100 105 110
 Pro Gly Phe Glu Ile Asn Phe Ile Lys Ser Gln Ser Ser Asn Met Leu
 115 120 125
 Thr Pro Tyr Asp Tyr Ser Ser Val Met His Tyr Gly Arg Leu Ala Phe
 130 135 140
 Ser Arg Arg Gly Leu Pro Thr Ile Thr Pro Leu Trp Ala Pro Ser Val
 145 150 155 160
 His Ile Gly Gln Arg Trp Asn Leu Ser Ala Ser Asp Ile Thr Arg Val
 165 170 175
 Leu Lys Leu Tyr Gly Cys
 180

<210> 60
 <211> 181
 <212> PRT
 <213> *Anguilla japonica*

<400> 60

Gly Leu Val Glu Val Pro Tyr Thr Val Ser Ser Glu Phe Ser Tyr Tyr
 1 5 10 15
 His Lys Lys Arg Ile Glu Asn Ala Met Glu Thr Phe Asn Thr Glu Thr
 20 25 30
 Cys Ile Arg Phe Val Pro Arg Ser Ser Gln Arg Asp Phe Ile Ser Ile
 35 40 45
 Glu Ser Arg Asp Gly Cys Tyr Ser Tyr Leu Gly Arg Thr Gly Gly Lys
 50 55 60
 Gln Val Val Ser Leu Ala Arg Tyr Gly Cys Val Tyr His Gly Ile Ile

4400>	61																	
tcttacc	atg	gag	ggt	gta	ggg	ggt	ctc	tgg	cct	tgg	gtg	ctg	ggt	ctg		49		
	Met	Glu	Gly	Val	Gly	Gly	Leu	Trp	Pro	Trp	Val	Leu	Gly	Leu				
	1				5					10								
ctc tcc	ttg	cca	ggt	gtg	atc	cta	gga	gcg	ccc	ctg	gcc	tcc	agc	tgc		97		
Leu	Ser	Leu	Pro	Gly	Val	Ile	Leu	Gly	Ala	Pro	Leu	Ala	Ser	Ser	Cys			
15				20					25				30					
gca gga	gcc	tgt	ggt	acc	agc	ttc	cca	gat	ggc	ctc	acc	cct	gag	gga		145		
Ala	Gly	Ala	Cys	Gly	Thr	Ser	Phe	Pro	Asp	Gly	Leu	Thr	Pro	Gly	Gly			
			35					40					45					
acc cag	gcc	tcc	ggg	gac	aag	gac	att	cct	gca	att	aac	caa	ggg	ctc		193		
Thr	Gln	Ala	Ser	Gly	Asp	Lys	Asp	Ile	Pro	Ala	Ile	Asn	Gln	Gly	Leu			
			50				55					60						
atc ctg	gaa	gaa	acc	cca	gag	agc	agc	ttc	ctc	atc	gag	ggg	gac	atc		241		
Ile	Leu	Glu	Glu	Thr	Pro	Glu	Ser	Ser	Phe	Leu	Ile	Glu	Gly	Asp	Ile			
	65					70					75							

atc cgg cgg agt ccc ttc cga ctg ctg tca gca acc agc aac aaa tgg Ile Arg Pro Ser Pro Phe Arg Leu Leu Ser Ala Thr Ser Asn Lys Trp 80 85 90	289
ccc atg ggt ggt agt ggt gtc gtg gag gtc ccc ttc ctg ctc tcc agc Pro Met Gly Gly Ser Gly Val Val Glu Val Pro Phe Leu Leu Ser Ser 95 100 105 110	337
aag tac gat gag ccc agc cgc cag gtc atc ctg gag gct ctt gcg gag Lys Tyr Asp Glu Pro Ser Arg Gln Val Ile Leu Glu Ala Leu Ala Glu 115 120 125	385
ttt gaa cgt tcc acg tgc atc agg ttt gtc acc tat cag gac cag aga Phe Glu Arg Ser Thr Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg 130 135 140	433
gac ttc att tcc atc atc ccc atg tat ggg tgc ttc tcg agt gtg ggg Asp Phe Ile Ser Ile Ile Pro Met Tyr Gly Cys Phe Ser Ser Val Gly 145 150 155	481
cgc agt gga ggg atg cag gtg gtc tcc ctg gcg ccc acg tgt ctc cag Arg Ser Gly Gly Met Gln Val Val Ser Leu Ala Pro Thr Cys Leu Gln 160 165 170	529
aag ggc cgg ggc att gtc ctt cat gag ctc atg cat gtg ctg ggc ttc Lys Gly Arg Gly Ile Val Leu His Glu Leu Met His Val Leu Gly Phe 175 180 185 190	577
tgg cac gag cac acg cgg gcc gac cgg gac cgc tat atc cgt gtc aac Trp His Glu His Thr Arg Ala Asp Arg Asp Arg Tyr Ile Arg Val Asn 195 200 205	625
tgg aac gag atc ctg cca gcc ttt gaa atc aac ttc atc aag tct cgg Trp Asn Glu Ile Leu Pro Gly Phe Glu Ile Asn Phe Ile Lys Ser Arg 210 215 220	673
agc agc aac atg ctg acg ccc tat gac tac tcc tct gtg atg cac tat Ser Ser Asn Met Leu Thr Pro Tyr Asp Tyr Ser Ser Val Met His Tyr 225 230 235	721
ggg agg ctc gcc ttc agc cgg cgt ggg ctg ccc acc atc aca cca ctt Gly Arg Leu Ala Phe Ser Arg Arg Gly Leu Pro Thr Ile Thr Pro Leu 240 245 250	769
tgg gcc ccc agt gtc cac atc gcc cag cga tgg aac ctg agt gcc tcg Trp Ala Pro Ser Val His Ile Gly Gln Arg Trp Asn Leu Ser Ala Ser 255 260 265 270	817
gac atc acc cgg gtc ctc aaa ctc tac ggc tgc agc cca agt gcc ccc Asp Ile Thr Arg Val Leu Lys Leu Tyr Gly Cys Ser Pro Ser Gly Pro 275 280 285	865
agg ccc cgt ggg aga ggg tcc cat gcc cac agc act ggt agg agc ccc Arg Pro Arg Gly Arg Gly Ser His Ala His Ser Thr Gly Arg Ser Pro 290 295 300	913

gct ccg gcc tcc cta tct ctg cag cgg ctt ttg gag gca ctg tcg gcg 961
 Ala Pro Ala Ser Leu Ser Leu Gln Arg Leu Leu Glu Ala Leu Ser Ala
 305 310 315

gaa tcc agg agc ccc gac ccc agt ggt tcc agt gcg gga ggc cag ccc 1009
 Glu Ser Arg Ser Pro Asp Pro Ser Gly Ser Ser Ala Gly Gly Gln Pro
 320 325 330

gtt cct gca ggg cct ggg gag agc cca cat ggg tgg gag tcc cct gcc 1057
 Val Pro Ala Gly Pro Gly Glu Ser Pro His Gly Trp Glu Ser Pro Ala
 335 340 345 350

ctg aaa aag ctg agt gca gag gcc tcg gca agg cag cct cag acc cta 1105
 Leu Lys Lys Leu Ser Ala Glu Ala Ser Ala Arg Gln Pro Gln Thr Leu
 355 360 365

gct tcc tcc cca aga tca agg cct gga gca ggt gcc ccc ggt gtt gct 1153
 Ala Ser Ser Pro Arg Ser Arg Pro Gly Ala Gly Ala Pro Gly Val Ala
 370 375 380

cag gag cag tcc tgg ctg gcc gga gtg tcc acc aag ccc aca gtc cca 1201
 Gln Glu Gln Ser Trp Leu Ala Gly Val Ser Thr Lys Pro Thr Val Pro
 385 390 395

tct tca gaa gca gga atc cag cca gtc cct gtc cag gga agc cca gct 1249
 Ser Ser Glu Ala Gly Ile Gln Pro Val Pro Val Gln Gly Ser Pro Ala
 400 405 410

ctg cca ggg ggc tgt gta cct aga aat cat ttc aag ggg atg tcc gaa 1297
 Leu Pro Gly Gly Cys Val Pro Arg Asn His Phe Lys Gly Met Ser Glu
 415 420 425 430

gat taagcctgtg gct 1313
 Asp

<210> 62
 <211> 230
 <212> PRT
 <213> Homo Sapiens

<400> 62
 Asp Lys Asp Ile Pro Ala Ile Asn Gln Gly Leu Ile Leu Glu Glu Thr
 1 5 10 15
 Pro Glu Ser Ser Phe Leu Ile Glu Gly Asp Ile Ile Arg Pro Ser Pro
 20 25 30
 Phe Arg Leu Leu Ser Ala Thr Ser Asn Lys Trp Pro Met Gly Gly Ser
 35 40 45
 Gly Val Val Glu Val Pro Phe Leu Leu Ser Ser Lys Tyr Asp Glu Pro

```

50              55              60
Ser Arg Gln Val Ile Leu Glu Ala Leu Ala Glu Phe Glu Arg Ser Thr
65              70              75              80

Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp Phe Ile Ser Ile
85              90              95

Ile Pro Met Tyr Gly Cys Phe Ser Ser Val Gly Arg Ser Gly Gly Met
100             105             110

Gln Val Val Ser Leu Ala Pro Thr Cys Leu Gln Lys Gly Arg Gly Ile
115             120             125

Val Leu His Glu Leu Met His Val Leu Gly Phe Trp His Glu His Thr
130             135             140

Arg Ala Asp Arg Asp Arg Tyr Ile Arg Val Asn Trp Asn Glu Ile Leu
145             150             155             160

Pro Gly Phe Glu Ile Asn Phe Ile Lys Ser Arg Ser Ser Asn Met Leu
165             170             175

Thr Pro Tyr Asp Tyr Ser Ser Val Met His Tyr Gly Arg Leu Ala Phe
180             185             190

Ser Arg Arg Gly Leu Pro Thr Ile Thr Pro Leu Trp Ala Pro Ser Val
195             200             205

His Ile Gly Gln Arg Trp Asn Leu Ser Ala Ser Asp Ile Thr Arg Val
210             215             220

Leu Lys Leu Tyr Gly Cys
225             230

<210> 63
<211> 179
<212> PRT
<213> Anguilla japonica

<400> 63

Asp Pro Asp Asp Leu Asp Ile Thr Ala Arg Ile Leu Gln Ser Asn Asn
1              5              10              15

Gly Ser Ser Glu Ile Leu Met Glu Gly Asp Met Val Val Ser Asn Thr
20             25             30

Arg Asn Ala Ile Asn Cys Trp Asn Asn Gln Cys Leu Trp Arg Lys Ser
35             40             45

Ser Asp Gly Leu Val Glu Val Pro Tyr Thr Val Ser Ser Glu Phe Ser
50             55             60

```

```

Tyr Tyr His Lys Lys Arg Ile Glu Asn Ala Met Glu Thr Phe Asn Thr
65              70              75              80

Glu Thr Cys Ile Arg Phe Val Pro Arg Ser Ser Gln Arg Asp Phe Ile
85              90              95

Ser Ile Glu Ser Arg Asp Gly Cys Tyr Ser Tyr Leu Gly Arg Thr Gly
100             105             110

Gly Lys Gln Val Val Ser Leu Ala Arg Tyr Gly Cys Val Tyr Pro Tyr
115             120             125

Asp Tyr Thr Ser Ile Met His Tyr Gly Arg Thr Ala Phe Ser Thr Asn
130             135             140

Gly Met Asp Thr Ile Thr Pro Val Pro Asn Pro Asn Gln Ser Ile Gly
145             150             155             160

Gln Arg Arg Ser Met Ser Lys Gly Asp Ile Leu Arg Ile Asn Lys Leu
165             170             175

```

Tyr Ser Cys

```

<210> 64
<211> 300
<212> PRT
<213> Homo Sapiens

```

<400> 64

```

Met Glu Gly Val Gly Gly Leu Trp Pro Trp Val Leu Gly Leu Leu Ser
1              5              10              15

Leu Pro Gly Val Ile Leu Gly Ala Pro Leu Ala Ser Ser Cys Ala Gly
20             25             30

Ala Cys Gly Thr Ser Phe Pro Asp Gly Leu Thr Pro Glu Gly Thr Gln
35             40             45

Ala Ser Gly Asp Lys Asp Ile Pro Ala Ile Asn Gln Gly Leu Ile Leu
50             55             60

Glu Glu Thr Pro Glu Ser Ser Phe Leu Ile Glu Gly Asp Ile Ile Arg
65             70             75             80

Pro Ser Pro Phe Arg Leu Leu Ser Ala Thr Ser Asn Lys Trp Pro Met
85             90             95

Gly Gly Ser Gly Val Val Glu Val Pro Phe Leu Leu Ser Ser Lys Tyr
100            105            110

Asp Glu Pro Ser Arg Gln Val Ile Leu Glu Ala Leu Ala Glu Phe Glu
115            120            125

```

```

Arg Ser Thr Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp Phe
 130                      135                      140
Ile Ser Ile Ile Pro Met Tyr Gly Cys Phe Ser Ser Val Gly Arg Ser
 145                      150                      155                      160
Gly Gly Met Gln Val Val Ser Leu Ala Pro Thr Cys Leu Gln Lys Gly
                      165                      170                      175
Arg Gly Ile Val Leu His Glu Leu Met His Val Leu Gly Phe Trp His
                      180                      185                      190
Glu His Thr Arg Ala Asp Arg Asp Arg Tyr Ile Arg Val Asn Trp Asn
 195                      200                      205
Glu Ile Leu Pro Gly Phe Glu Ile Asn Phe Ile Lys Ser Arg Ser Ser
 210                      215                      220
Asn Met Leu Thr Pro Tyr Asp Tyr Ser Ser Val Met His Tyr Gly Arg
 225                      230                      235                      240
Leu Ala Phe Ser Arg Arg Gly Leu Pro Thr Ile Thr Pro Leu Trp Ala
                      245                      250                      255
Pro Ser Val His Ile Gly Gln Arg Trp Asn Leu Ser Ala Ser Asp Ile
 260                      265                      270
Thr Arg Val Leu Lys Leu Tyr Gly Cys Ser Pro Ser Gly Pro Arg Pro
 275                      280                      285
Arg Gly Arg Gly Glu Trp His Gly Arg Lys Val Thr
 290                      295                      300

```

```

<210> 65
<211> 436
<212> PRT
<213> Homo Sapiens

```

```

<400> 65
Met Ser Cys Cys Leu Val Ser Pro Val Gly Ala Pro Gly Ile Cys Val
 1                      5                      10                      15
Cys Pro Cys Leu Ser Gly Pro Gly Val Ile Leu Gly Ala Pro Leu Ala
 20                      25                      30
Ser Ser Cys Ala Gly Ala Cys Gly Thr Ser Phe Pro Asp Gly Leu Thr
 35                      40                      45
Pro Glu Gly Thr Gln Ala Ser Gly Asp Lys Asp Ile Pro Ala Ile Asn
 50                      55                      60
Gln Gly Leu Ile Leu Glu Glu Thr Pro Glu Ser Ser Phe Leu Ile Glu

```

65		70		75		80
Gly Asp Ile Ile Arg Pro Ser Pro Phe Arg Leu Leu Ser Ala Thr Ser						
	85			90		95
Asn Lys Trp Pro Met Gly Gly Ser Gly Val Val Glu Val Pro Phe Leu						
	100		105			110
Leu Ser Ser Lys Tyr Asp Glu Pro Ser Arg Gln Val Ile Leu Glu Ala						
	115		120			125
Leu Ala Glu Phe Glu Arg Ser Thr Cys Ile Arg Phe Val Thr Tyr Gln						
	130		135			140
Asp Gln Arg Asp Phe Ile Ser Ile Ile Pro Met Tyr Gly Cys Phe Ser						
	145		150		155	160
Ser Val Gly Arg Ser Gly Gly Met Gln Val Val Ser Leu Ala Pro Thr						
		165		170		175
Cys Leu Gln Lys Gly Arg Gly Ile Val Leu His Glu Leu Met His Val						
	180			185		190
Leu Gly Phe Trp His Glu His Thr Arg Ala Asp Arg Asp Arg Tyr Ile						
	195			200		205
Arg Val Asn Trp Asn Glu Ile Leu Pro Gly Phe Glu Ile Asn Phe Ile						
	210		215			220
Lys Ser Arg Ser Ser Asn Met Leu Thr Pro Tyr Asp Tyr Ser Ser Val						
	225		230		235	240
Met His Tyr Gly Arg Leu Ala Phe Ser Arg Arg Gly Leu Pro Thr Ile						
		245		250		255
Thr Pro Leu Trp Ala Pro Ser Val His Ile Gly Gln Arg Trp Asn Leu						
		260		265		270
Ser Ala Ser Asp Ile Thr Arg Val Leu Lys Leu Tyr Gly Cys Ser Pro						
	275		280			285
Ser Gly Pro Arg Pro Arg Gly Arg Gly Ser His Ala His Ser Thr Gly						
	290		295			300
Arg Ser Pro Ala Pro Ala Ser Leu Ser Leu Gln Arg Leu Leu Glu Ala						
	305		310		315	320
Leu Ser Ala Glu Ser Arg Ser Pro Asp Pro Ser Gly Ser Ser Ala Gly						
		325		330		335
Gly Gln Pro Val Pro Ala Gly Pro Gly Glu Ser Pro His Gly Trp Glu						
	340			345		350
Ser Pro Ala Leu Lys Lys Leu Ser Ala Glu Ala Ser Ala Arg Gln Pro						
	355		360			365

Gln Thr Leu Ala Ser Ser Pro Arg Ser Arg Pro Gly Ala Gly Ala Pro
 370 375 380

Gly Val Ala Gln Glu Gln Ser Trp Leu Ala Gly Val Ser Thr Lys Pro
 385 390 395 400

Thr Val Pro Ser Ser Glu Ala Gly Ile Gln Pro Val Pro Val Gln Gly
 405 410 415

Ser Pro Ala Leu Pro Gly Gly Cys Val Pro Arg Asn His Phe Lys Gly
 420 425 430

Met Ser Glu Asp
 435

<210> 66
 <211> 188
 <212> PRT
 <213> Homo Sapiens

<400> 66

Trp Pro Met Gly Gly Ser Gly Val Val Glu Val Pro Phe Leu Leu Ser
 1 5 10 15

Ser Lys Tyr Asp Glu Pro Ser His Gln Val Ile Leu Glu Ala Leu Ala
 20 25 30

Glu Phe Glu Arg Ser Thr Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln
 35 40 45

Arg Asp Phe Ile Ser Ile Ile Pro Met Tyr Gly Cys Phe Ser Ser Val
 50 55 60

Gly Arg Ser Gly Gly Met Gln Val Val Ser Leu Ala Pro Thr Cys Leu
 65 70 75 80

Gln Lys Gly Arg Gly Ile Val Leu His Glu Leu Met His Val Leu Gly
 85 90 95

Phe Trp His Glu His Thr Arg Ala Asp Arg Asp Arg Tyr Ile Arg Val
 100 105 110

Asn Trp Asn Glu Ile Leu Pro Gly Phe Glu Ile Asn Phe Ile Lys Ser
 115 120 125

Gln Ser Ser Asn Met Leu Thr Pro Tyr Asp Tyr Ser Ser Val Met His
 130 135 140

Tyr Gly Arg Leu Ala Phe Ser Arg Arg Gly Leu Pro Thr Ile Thr Pro
 145 150 155 160

Leu Trp Ala Pro Ser Val His Ile Gly Gln Arg Trp Asn Leu Ser Ala

165 170 175

Ser Asp Ile Thr Arg Val Leu Lys Leu Tyr Gly Cys

180 185